

SEQUENCE LISTING

IAP5 Rec'd PCT/PTO 10 FEB 2006

<110> TAKARA BIO INC.

<120> Method of decomposing dsRNA and synthesizing RNA

<130> 664674

<150> JP 2003-293553

<151> 2003-08-14

<150> JP 2003-342126

<151> 2003-09-30

<150> JP 2003-409639

<151> 2003-12-08

<150> JP 2004-086129

<151> 2004-03-24

<160> 27

<170> PatentIn version 3.1

<210> 1

<211> 1924

<212> PRT

<213> Homo sapiens

<400> 1

Met Lys Ser Pro Ala Leu Gln Pro Leu Ser Met Ala Gly Leu Gln Leu
 1 5 10 15

Met Thr Pro Ala Ser Ser Pro Met Gly Pro Phe Phe Gly Leu Pro Trp
 20 25 30

Gln Gln Glu Ala Ile His Asp Asn Ile Tyr Thr Pro Arg Lys Tyr Gln
 35 40 45

Val Glu Leu Leu Glu Ala Ala Leu Asp His Asn Thr Ile Val Cys Leu
 50 55 60

Asn Thr Gly Ser Gly Lys Thr Phe Ile Ala Ser Thr Thr Leu Leu Lys
 65 70 75 80

Ser Cys Leu Tyr Leu Asp Leu Gly Glu Thr Ser Ala Arg Asn Gly Lys

664674description (1)Sequence Listing

85

90

95

Arg Thr Val Phe Leu Val Asn Ser Ala Asn Gln Val Ala Gln Gln Val
 100 105 110

Ser Ala Val Arg Thr His Ser Asp Leu Lys Val Gly Glu Tyr Ser Asn
 115 120 125

Leu Glu Val Asn Ala Ser Trp Thr Lys Glu Arg Trp Asn Gln Glu Phe
 130 135 140

Thr Lys His Gln Val Leu Ile Met Thr Cys Tyr Val Ala Leu Asn Val
 145 150 155 160

Leu Lys Asn Gly Tyr Leu Ser Leu Ser Asp Ile Asn Leu Leu Val Phe
 165 170 175

Asp Glu Cys His Leu Ala Ile Leu Asp His Pro Tyr Arg Glu Phe Met
 180 185 190

Lys Leu Cys Glu Ile Cys Pro Ser Cys Pro Arg Ile Leu Gly Leu Thr
 195 200 205

Ala Ser Ile Leu Asn Gly Lys Trp Asp Pro Glu Asp Leu Glu Glu Lys
 210 215 220

Phe Gln Lys Leu Glu Lys Ile Leu Lys Ser Asn Ala Glu Thr Ala Thr
 225 230 235 240

Asp Leu Val Val Leu Asp Arg Tyr Thr Ser Gln Pro Cys Glu Ile Val
 245 250 255

Val Asp Cys Gly Pro Phe Thr Asp Arg Ser Gly Leu Tyr Glu Arg Leu
 260 265 270

Leu Met Glu Leu Glu Glu Ala Leu Asn Phe Ile Asn Asp Cys Asn Ile
 275 280 285

Ser Val His Ser Lys Glu Arg Asp Ser Thr Leu Ile Ser Lys Gln Ile
 290 295 300

Leu Ser Asp Cys Arg Ala Val Leu Val Val Leu Gly Pro Trp Cys Ala

664674description (1)Sequence Listing

305 310 315 320

Asp Lys Val Ala Gly Met Met Val Arg Glu Leu Gln Lys Tyr Ile Lys
325 330 335

His Glu Gln Glu Glu Leu His Arg Lys Phe Leu Leu Phe Thr Asp Thr
340 345 350

Phe Leu Arg Lys Ile His Ala Leu Cys Glu Glu His Phe Ser Pro Ala
355 360 365

Ser Leu Asp Leu Lys Phe Val Thr Pro Lys Val Ile Lys Leu Leu Glu
370 375 380

Ile Leu Arg Lys Tyr Lys Pro Tyr Glu Arg His Ser Phe Glu Ser Val
385 390 395 400

Glu Trp Tyr Asn Asn Arg Asn Gln Asp Asn Tyr Val Ser Trp Ser Asp
405 410 415

Ser Glu Asp Asp Asp Glu Asp Glu Glu Ile Glu Glu Lys Glu Lys Pro
420 425 430

Glu Thr Asn Phe Pro Ser Pro Phe Thr Asn Ile Leu Cys Gly Ile Ile
435 440 445

Phe Val Glu Arg Arg Tyr Thr Ala Val Val Leu Asn Arg Leu Ile Lys
450 455 460

Glu Ala Gly Lys Gln Asp Pro Glu Leu Ala Tyr Ile Ser Ser Asn Phe
465 470 475 480

Ile Thr Gly His Gly Ile Gly Lys Asn Gln Pro Arg Asn Asn Thr Met
485 490 495

Glu Ala Glu Phe Arg Lys Gln Glu Glu Val Leu Arg Lys Phe Arg Ala
500 505 510

His Glu Thr Asn Leu Leu Ile Ala Thr Ser Ile Val Glu Glu Gly Val
515 520 525

Asp Ile Pro Lys Cys Asn Leu Val Val Arg Phe Asp Leu Pro Thr Glu

664674description (1)Sequence Listing

530

535

540

Tyr Arg Ser Tyr Val Gln Ser Lys Gly Arg Ala Arg Ala Pro Ile Ser
 545 550 555 560

Asn Tyr Ile Met Leu Ala Asp Thr Asp Lys Ile Lys Ser Phe Glu Glu
 565 570 575

Asp Leu Lys Thr Tyr Lys Ala Ile Glu Lys Ile Leu Arg Asn Lys Cys
 580 585 590

Ser Lys Ser Val Asp Thr Gly Glu Thr Asp Ile Asp Pro Val Met Asp
 595 600 605

Asp Asp His Val Phe Pro Pro Tyr Val Leu Arg Pro Asp Asp Gly Gly
 610 615 620

Pro Arg Val Thr Ile Asn Thr Ala Ile Gly His Ile Asn Arg Tyr Cys
 625 630 635 640

Ala Arg Leu Pro Ser Asp Pro Phe Thr His Leu Ala Pro Lys Cys Arg
 645 650 655

Thr Arg Glu Leu Pro Asp Gly Thr Phe Tyr Ser Thr Leu Tyr Leu Pro
 660 665 670

Ile Asn Ser Pro Leu Arg Ala Ser Ile Val Gly Pro Pro Met Ser Cys
 675 680 685

Val Arg Leu Ala Glu Arg Val Val Ala Leu Ile Cys Cys Glu Lys Leu
 690 695 700

His Lys Ile Gly Glu Leu Asp Asp His Leu Met Pro Val Gly Lys Glu
 705 710 715 720

Thr Val Lys Tyr Glu Glu Glu Leu Asp Leu His Asp Glu Glu Glu Thr
 725 730 735

Ser Val Pro Gly Arg Pro Gly Ser Thr Lys Arg Arg Gln Cys Tyr Pro
 740 745 750

Lys Ala Ile Pro Glu Cys Leu Arg Asp Ser Tyr Pro Arg Pro Asp Gln
 ページ(4)

664674description (1)Sequence Listing

755

760

765

Pro Cys Tyr Leu Tyr Val Ile Gly Met Val Leu Thr Thr Pro Leu Pro
770 775 780

Asp Glu Leu Asn Phe Arg Arg Arg Lys Leu Tyr Pro Pro Glu Asp Thr
785 790 795 800

Thr Arg Cys Phe Gly Ile Leu Thr Ala Lys Pro Ile Pro Gln Ile Pro
805 810 815

His Phe Pro Val Tyr Thr Arg Ser Gly Glu Val Thr Ile Ser Ile Glu
820 825 830

Leu Lys Lys Ser Gly Phe Met Leu Ser Leu Gln Met Leu Glu Leu Ile
835 840 845

Thr Arg Leu His Gln Tyr Ile Phe Ser His Ile Leu Arg Leu Glu Lys
850 855 860

Pro Ala Leu Glu Phe Lys Pro Thr Asp Ala Asp Ser Ala Tyr Cys Val
865 870 875 880

Leu Pro Leu Asn Val Val Asn Asp Ser Ser Thr Leu Asp Ile Asp Phe
885 890 895

Lys Phe Met Glu Asp Ile Glu Lys Ser Glu Ala Arg Ile Gly Ile Pro
900 905 910

Ser Thr Lys Tyr Thr Lys Glu Thr Pro Phe Val Phe Lys Leu Glu Asp
915 920 925

Tyr Gln Asp Ala Val Ile Ile Pro Arg Tyr Arg Asn Phe Asp Gln Pro
930 935 940

His Arg Phe Tyr Val Ala Asp Val Tyr Thr Asp Leu Thr Pro Leu Ser
945 950 955 960

Lys Phe Pro Ser Pro Glu Tyr Glu Thr Phe Ala Glu Tyr Tyr Lys Thr
965 970 975

Lys Tyr Asn Leu Asp Leu Thr Asn Leu Asn Gln Pro Leu Leu Asp Val

664674description (1)Sequence Listing

980

985

990

Asp His Thr Ser Ser Arg Leu Asn Leu Leu Thr Pro Arg His Leu Asn
995 1000 1005

Gln Lys Gly Lys Ala Leu Pro Leu Ser Ser Ala Glu Lys Arg Lys
1010 1015 1020

Ala Lys Trp Glu Ser Leu Gln Asn Lys Gln Ile Leu Val Pro Glu
1025 1030 1035

Leu Cys Ala Ile His Pro Ile Pro Ala Ser Leu Trp Arg Lys Ala
1040 1045 1050

Val Cys Leu Pro Ser Ile Leu Tyr Arg Leu His Cys Leu Leu Thr
1055 1060 1065

Ala Glu Glu Leu Arg Ala Gln Thr Ala Ser Asp Ala Gly Val Gly
1070 1075 1080

Val Arg Ser Leu Pro Ala Asp Phe Arg Tyr Pro Asn Leu Asp Phe
1085 1090 1095

Gly Trp Lys Lys Ser Ile Asp Ser Lys Ser Phe Ile Ser Ile Ser
1100 1105 1110

Asn Ser Ser Ser Ala Glu Asn Asp Asn Tyr Cys Lys His Ser Thr
1115 1120 1125

Ile Val Pro Glu Asn Ala Ala His Gln Gly Ala Asn Arg Thr Ser
1130 1135 1140

Ser Leu Glu Asn His Asp Gln Met Ser Val Asn Cys Arg Thr Leu
1145 1150 1155

Leu Ser Glu Ser Pro Gly Lys Leu His Val Glu Val Ser Ala Asp
1160 1165 1170

Leu Thr Ala Ile Asn Gly Leu Ser Tyr Asn Gln Asn Leu Ala Asn
1175 1180 1185

Gly Ser Tyr Asp Leu Ala Asn Arg Asp Phe Cys Gln Gly Asn Gln

664674description (1)Sequence Listing

1190		1195		1200
Leu Asn Tyr Tyr Lys Gln Glu Ile Pro Val Gln Pro Thr Thr Ser	1205	1210	1215	
Tyr Ser Ile Gln Asn Leu Tyr Ser Tyr Glu Asn Gln Pro Gln Pro	1220	1225	1230	
Ser Asp Glu Cys Thr Leu Leu Ser Asn Lys Tyr Leu Asp Gly Asn	1235	1240	1245	
Ala Asn Lys Ser Thr Ser Asp Gly Ser Pro Val Met Ala Val Met	1250	1255	1260	
Pro Gly Thr Thr Asp Thr Ile Gln Val Leu Lys Gly Arg Met Asp	1265	1270	1275	
Ser Glu Gln Ser Pro Ser Ile Gly Tyr Ser Ser Arg Thr Leu Gly	1280	1285	1290	
Pro Asn Pro Gly Leu Ile Leu Gln Ala Leu Thr Leu Ser Asn Ala	1295	1300	1305	
Ser Asp Gly Phe Asn Leu Glu Arg Leu Glu Met Leu Gly Asp Ser	1310	1315	1320	
Phe Leu Lys His Ala Ile Thr Thr Tyr Leu Phe Cys Thr Tyr Pro	1325	1330	1335	
Asp Ala His Glu Gly Arg Leu Ser Tyr Met Arg Ser Lys Lys Val	1340	1345	1350	
Ser Asn Cys Asn Leu Tyr Arg Leu Gly Lys Lys Lys Gly Leu Pro	1355	1360	1365	
Ser Arg Met Val Val Ser Ile Phe Asp Pro Pro Val Asn Trp Leu	1370	1375	1380	
Pro Pro Gly Tyr Val Val Asn Gln Asp Lys Ser Asn Thr Asp Lys	1385	1390	1395	
Trp Glu Lys Asp Glu Met Thr Lys Asp Cys Met Leu Ala Asn Gly				

664674description (1)Sequence Listing

1400		1405		1410
Lys Leu Asp Glu Asp Tyr Glu Glu Glu Asp Glu Glu Glu Glu Ser	1415	1420		1425
Leu Met Trp Arg Ala Pro Lys Glu Glu Ala Asp Tyr Glu Asp Asp	1430	1435		1440
Phe Leu Glu Tyr Asp Gln Glu His Ile Arg Phe Ile Asp Asn Met	1445	1450		1455
Leu Met Gly Ser Gly Ala Phe Val Lys Lys Ile Ser Leu Ser Pro	1460	1465		1470
Phe Ser Thr Thr Asp Ser Ala Tyr Glu Trp Lys Met Pro Lys Lys	1475	1480		1485
Ser Ser Leu Gly Ser Met Pro Phe Ser Ser Asp Phe Glu Asp Phe	1490	1495		1500
Asp Tyr Ser Ser Trp Asp Ala Met Cys Tyr Leu Asp Pro Ser Lys	1505	1510		1515
Ala Val Glu Glu Asp Asp Phe Val Val Gly Phe Trp Asn Pro Ser	1520	1525		1530
Glu Glu Asn Cys Gly Val Asp Thr Gly Lys Gln Ser Ile Ser Tyr	1535	1540		1545
Asp Leu His Thr Glu Gln Cys Ile Ala Asp Lys Ser Ile Ala Asp	1550	1555		1560
Cys Val Glu Ala Leu Leu Gly Cys Tyr Leu Thr Ser Cys Gly Glu	1565	1570		1575
Arg Ala Ala Gln Leu Phe Leu Cys Ser Leu Gly Leu Lys Val Leu	1580	1585		1590
Pro Val Ile Lys Arg Thr Asp Arg Glu Lys Ala Leu Cys Pro Thr	1595	1600		1605

664674description (1)Sequence Listing

Arg	Glu	Asn	Phe	Asn	Ser	Gln	Gln	Lys	Asn	Leu	Ser	Val	Ser	Cys
1610						1615					1620			
Ala	Ala	Ala	Ser	Val	Ala	Ser	Ser	Arg	Ser	Ser	Val	Leu	Lys	Asp
1625						1630					1635			
Ser	Glu	Tyr	Gly	Cys	Leu	Lys	Ile	Pro	Pro	Arg	Cys	Met	Phe	Asp
1640						1645					1650			
His	Pro	Asp	Ala	Asp	Lys	Thr	Leu	Asn	His	Leu	Ile	Ser	Gly	Phe
1655						1660					1665			
Glu	Asn	Phe	Glu	Lys	Lys	Ile	Asn	Tyr	Arg	Phe	Lys	Asn	Lys	Ala
1670						1675					1680			
Tyr	Leu	Leu	Gln	Ala	Phe	Thr	His	Ala	Ser	Tyr	His	Tyr	Asn	Thr
1685						1690					1695			
Ile	Thr	Asp	Cys	Tyr	Gln	Arg	Leu	Glu	Phe	Leu	Gly	Asp	Ala	Ile
1700						1705					1710			
Leu	Asp	Tyr	Leu	Ile	Thr	Lys	His	Leu	Tyr	Glu	Asp	Pro	Arg	Gln
1715						1720					1725			
His	Ser	Pro	Gly	Val	Leu	Thr	Asp	Leu	Arg	Ser	Ala	Leu	Val	Asn
1730						1735					1740			
Asn	Thr	Ile	Phe	Ala	Ser	Leu	Ala	Val	Lys	Tyr	Asp	Tyr	His	Lys
1745						1750					1755			
Tyr	Phe	Lys	Ala	Val	Ser	Pro	Glu	Leu	Phe	His	Val	Ile	Asp	Asp
1760						1765					1770			
Phe	Val	Gln	Phe	Gln	Leu	Glu	Lys	Asn	Glu	Met	Gln	Gly	Met	Asp
1775						1780					1785			
Ser	Glu	Leu	Arg	Arg	Ser	Glu	Glu	Asp	Glu	Glu	Lys	Glu	Glu	Asp
1790						1795					1800			
Ile	Glu	Val	Pro	Lys	Ala	Met	Gly	Asp	Ile	Phe	Glu	Ser	Leu	Ala
1805						1810					1815			

664674description (1)Sequence Listing

Gly Ala Ile Tyr Met Asp Ser Gly Met Ser Leu Glu Thr Val Trp
1820 1825 1830

Gln Val Tyr Tyr Pro Met Met Arg Pro Leu Ile Glu Lys Phe Ser
1835 1840 1845

Ala Asn Val Pro Arg Ser Pro Val Arg Glu Leu Leu Glu Met Glu
1850 1855 1860

Pro Glu Thr Ala Lys Phe Ser Pro Ala Glu Arg Thr Tyr Asp Gly
1865 1870 1875

Lys Val Arg Val Thr Val Glu Val Val Gly Lys Gly Lys Phe Lys
1880 1885 1890

Gly Val Gly Arg Ser Tyr Arg Ile Ala Lys Ser Ala Ala Ala Arg
1895 1900 1905

Arg Ala Leu Arg Ser Leu Lys Ala Asn Gln Pro Gln Val Pro Asn
1910 1915 1920

Ser

<210> 2
<211> 5772
<212> DNA
<213> Homo sapiens

<400> 2
atgaaaagcc ctgctttgca acccctcagc atggcaggcc tgcagctcat gacccctgct 60
tcctcaccaa tgggtccttt ctttggactg ccatggcaac aagaagcaat tcataataac 120
atttatacgc caagaaaata tcaggttgaa ctgcttgaag cagctctgga tcataataacc 180
atcgtctggt taaacactgg ctgagggaag acatttattg ctagtactac tctactaaag 240
agctgtctct atctagatct aggggagact tcagctagaa atggaaaaag gacgggtgttc 300
ttggtcaact ctgcaaacca ggttgcgtcaa caagtgtcag ctgtcagaac tcattcagat 360
ctcaagggtg gggaatactc aaacctagaa gtaaattgat cttggacaaa agagagatgg 420
aaccaagagt ttactaagca ccaggttctc attatgactt gctatgtcgc cttgaatgtt 480
ttgaaaaatg gttacttata actgtcagac attaaccttt tgggtgttga tgagtgtcat 540

664674description (1)Sequence Listing

cttgcaatcc tagaccaccc ctatcgagaa tttatgaagc tctgtgaaat ttgtccatca	600
tgtcctcgca ttttgggact aactgcttcc attttaaatg ggaaatggga tccagaggat	660
ttggaagaaa agtttcagaa actagagaaa attcttaaga gtaatgctga aactgcaact	720
gacctggtgg tottagacag gtatacttct cagccatgtg agattgtggt ggattgtgga	780
ccattttactg acagaagtgg gctttatgaa agactgctga tggaattaga agaagcactt	840
aattttatca atgattgtaa tatactgtga cattcaaaag aaagagattc tactttaatt	900
togaaacaga tactatcaga ctgtcgtgcc gtattggtag ttctgggacc ctggtgtgca	960
gataaagtag ctggaatgat ggtaagagaa ctacagaaat acatcaaaca tgagcaagag	1020
gagctgcaca ggaaattttt attgtttaca gacactttcc taaggaaaat acatgcacta	1080
tgtgaagagc acttctcacc tgcctcactt gacctgaaat ttgtaactcc taaagtaatc	1140
aaactgctcg aaatcttacg caaatataaa ccatatgagc gacacagttt tgaaagcgtt	1200
gagtgggtata ataatagaaa tcaggataat tatgtgtcat ggagtgattc tgaggatgat	1260
gatgaggatg aagaaattga agaaaaagag aagccagaga caaattttcc ttctcctttt	1320
accaacattt tgtgcggaat tatttttgtg gaaagaagat acacagcagt tgtcttaaac	1380
agattgataa aggaagctgg caaacaagat ccagagctgg cttatatcag tagcaatttc	1440
ataactggac atggcattgg gaagaatcag cctcgcaaca acacgatgga agcagaattc	1500
agaaaacagg aagaggtact taggaaattt cgagcacatg agaccaacct gottattgca	1560
acaagtattg tagaagaggg tgttgatata ccaaaatgca acttggtggt tegtittgat	1620
ttgccacag aatatcgatc ctatgttcaa tctaaaggaa gagcaagggc acccatctct	1680
aattatataa tgttagcgga tacagacaaa ataaaaagtt ttgaagaaga ccttaaaacc	1740
tacaaagcta ttgaaaagat cttgagaaac aagtgttcca agtcggttga tactggtgag	1800
actgacattg atcctgtcat ggatgatgat cacgttttcc caccatatgt gttgaggcct	1860
gacgatggtg gtccacgagt cacaatcaac acggccattg gacacatcaa tagatactgt	1920
gctagattac caagtgatcc gtttactcat ctagctccta aatgcagaac ccgagagttg	1980
cctgatggta cattttattc aactctttat ctgccaatca actcacctct tcgagcctcc	2040
attgttggtc caccaatgag ctgtgtacga ttggctgaaa gagttgtcgc tctcatttgc	2100
tgtgagaaac tgcacaaaat tggcgaactg gatgaccatt tgatgccagt tgggaaagag	2160
actgttaaat atgaagagga gcttgatttg catgatgaag aagagaccag tgttccagga	2220

664674description (1)Sequence Listing

agaccagggtt ccaogaaacg aaggcagtgc tacccaaaag caattccaga gtgtttgagg	2280
gatagttatc ccagacctga tcagccctgt tacctgtatg tgataggaat ggttttaact	2340
acacctttac ctgatgaact caactttaga aggcggaagc tctatcctcc tgaagatacc	2400
acaagatgct ttggaatact gacggccaaa cccatacctc agattccaca ctttcctgtg	2460
tacacacgct ctggagaggt taccatatcc attgagtiga agaagtctgg tttcatgttg	2520
tctctacaaa tgcttgagtt gattacaaga cttcaccagt atatattctc acatattctt	2580
cggcttgaaa aacctgcact agaatttaaa cctacagacg ctgattcagc atactgtgtt	2640
ctaccttta atgttggttaa tgactccagc actttggata ttgactttaa attcatggaa	2700
gatattgaga agtctgaagc tcgcataggc attcccagta caaagtatac aaaagaaaca	2760
ccctttgttt ttaaattaga agattaccaa gatgccgtta tcattccaag atatcgcaat	2820
tttgatcagc ctcatcgatt ttatgtagct gatgtgtaca ctgatcttac cccactcagt	2880
aaatttcctt cccctgagta tgaaactttt gcagaatatt ataaaacaaa gtacaacctt	2940
gacctaacca atctcaacca gccactgctg gatgtggacc acacatcttc aagacttaat	3000
cttttgacac ctcgacattt gaatcagaag gggaaagcgc ttcctttaag cagtgtgag	3060
aagaggaaag ccaaattggga aagtctgcag aataaacaga tactggttcc agaactctgt	3120
gctatacatc caattccagc atcactgtgg agaaaagctg tttgtctccc cagcatactt	3180
tatcgccttc actgcctttt gactgcagag gagctaagag cccagactgc cagcgatgct	3240
ggcgtgggag tcagatcact tcctgcggat tttagatacc ctaacttaga cttcgggttg	3300
aaaaaatcta ttgacagcaa atctttcatc tcaatttcta actcctcttc agctgaaaat	3360
gataattact gtaagcacag cacaattgtc cctgaaaatg ctgcacatca aggtgcta	3420
agaacctcct ctctagaaaa tcatgaccaa atgtctgtga actgcagaac gttgctcagc	3480
gagtcccctg gtaagctcca cgttgaagtt tcagcagatc ttacagcaat taatggtctt	3540
tottacaatc aaaatctcgc caatggcagt tatgatttag ctaacagaga cttttgccaa	3600
ggaaatcagc taaattacta caagcaggaa ataccctgac aaccaactac ctcatattcc	3660
attcagaatt tatacagtta cgagaaccag cccagccca gcgatgaatg tactctcctg	3720
agtaataaat accttgatgg aaatgctaac aaatctacct cagatggaag tcctgtgatg	3780
gcgtaaatgc ctggtacgac agacactatt caagtgtca agggcaggat ggattctgag	3840
cagagccctt ctattgggta ctctcaagg actcttgcc ccaatcctgg acttattctt	3900

664674description (1)Sequence Listing

caggctttga ctctgtcaaa cgctagtgat ggatttaacc tggagcggct tgaaatgctt	3960
ggcgactcct ttttaaagca tgccatcacc acatatctat tttgcactta cctgatgog	4020
catgagggcc gcctttcata tatgagaagc aaaaaggcca gcaactgtaa tctgtatcgc	4080
cttggaaaaa agaagggact acccagccgc atgggtggtgt caatatttga tccccctgtg	4140
aattggcttc ctcttggtta tgtagtaa at caagacaaaa gcaacacaga taaatgggaa	4200
aaagatgaaa tgacaaaaga ctgcatgctg gcgaatggca aactggatga ggattacgag	4260
gaggaggatg aggaggagga gagcctgatg tggagggctc cgaaggaaga ggctgactat	4320
gaagatgatt tcctggagta tgatcaggaa catatcagat ttatagataa tatgttaatg	4380
gggtcaggag cttttgtaaa gaaaatctct ctttctcctt tttcaaccac tgattctgca	4440
tatgaatgga aaatgccccaa aaaatcctcc ttaggtagta tgccattttc atcagatttt	4500
gaggattttg actacagctc ttgggatgca atgtgctatc tggatcctag caaagctgtt	4560
gaagaagatg actttgtggt ggggttctgg aatccatcag aagaaaactg tgggtgtgac	4620
acgggaaagc agtccatttc ttacgacttg cacactgagc agtgtattgc tgacaaaagc	4680
atagcggact gtgtggaagc cctgctgggc tgctatttaa ccagctgtgg ggagagggct	4740
gctcagcttt tcctctgttc actggggctg aagggtgctcc cggttaattaa aaggactgat	4800
cgggaaaagg ccctgtgccc tactogggag aatttcaaca gccaaacaaa gaacctttca	4860
gtgagctgtg ctgctgcttc tgtggccagt tcacgctctt ctgtattgaa agactcggaa	4920
tatggttggt tgaagattcc accaagatgt atgtttgatc atccagatgc agataaaaca	4980
ctgaatcacc ttatatcggg gtttgaaaat ttgaaaaga aaatcaacta cagattcaag	5040
aataaggctt accttctcca ggcttttaca catgcctcct accactacaa tactatcact	5100
gattgttacc agcgcttaga attcctggga gatgcgattt tggactacct cataaccaag	5160
cacctttatg aagaccgcgc gcagcactcc ccgggggtcc tgacagacct gcggtctgcc	5220
ctggtcaaca acaccatctt tgcatogctg gctgtaaagt acgactacca caagtacttc	5280
aaagctgtct ctctgagct cttccatgtc attgatgact ttgtgcagtt tcagottgag	5340
aagaatgaaa tgcaaggaat ggattctgag cttaggagat ctgaggagga tgaagagaaa	5400
gaagaggata ttgaagttcc aaaggccatg ggggatattt ttgagtcgct tgctgggtgcc	5460
atttacatgg atagtgggat gtcactggag acagtctggc aggtgtacta tcccatgatg	5520
cggccactaa tagaaaagtt ttctgcaa at gtaccccggt cccctgtgog agaattgctt	5580

664674description (1)Sequence Listing

gaaatggaac cagaaactgc caaatitagc cggctgaga gaacttacga cggaaggtc	5640
agagtactg tggaagtagt aggaaaggg aaatttaaag gtgttggtcg aagttacagg	5700
attgccaaat ctgcagcagc aagaagagcc ctccgaagcc tcaaagctaa tcaacctcag	5760
gttcccaata gc	5772

<210> 3
 <211> 1962
 <212> DNA
 <213> Artificial sequence

<220>
 <223> A gene encoding human dicer mutant

<400> 3	
caagtgtca agggcaggat ggattctgag cagagccctt ctattgggta ctctcaagg	60
actcttgcc ccaatcctgg acttattctt caggctttga ctctgtcaaa cgctagtgt	120
ggatttaacc tggagcggct tgaaatgctt ggcgactcct ttttaaagca tgccatcacc	180
acatatctat tttgcaacta ccctgatgcg catgagggcc gcctttcata tatgagaagc	240
aaaaaggtca gcaactgtaa tctgtatcgc cttggaaaaa agaagggact acccagccgc	300
atggtggtgt caatatttga tccccctgtg aattggcttc ctcttggtta ttagtaaat	360
caagacaaaa gcaacacaga taaatgggaa aaagatgaaa tgacaaaaga ctgcatgctg	420
gcgaatggca aactggatga ggattacgag gaggaggatg aggaggagga gagcctgatg	480
tggagggctc cgaaggaaga ggctgactat gaagatgatt tcctggagta tgatcaggaa	540
catatcagat ttatagataa tatgttaatg gggtcaggag cttttgtaaa gaaaatctct	600
ctttctcctt tttcaaccac tgattctgca tatgaatgga aaatgcccac aaaatcctcc	660
ttaggtagta tgccattttc atcagatttt gaggattttg actacagctc ttgggatgca	720
atgtgctatc tggatcctag caaagctgtt gaagaagatg actttgttgt ggggttctgg	780
aatccatcag aagaaaactg tgggtgtgac acgggaaagc agtccatttc ttacgacttg	840
cacactgagc agtgtattgc tgacaaaagc atagcggact gtgtggaagc cctgctgggc	900
tgctatttaa ccagctgtgg ggagagggt gctcagcttt tcctctgttc actggggctg	960
aaggtgctcc cggtaattaa aaggactgat cgggaaaagg ccctgtgccc tactcgggag	1020
aatttcaaca gccacaaaa gaacctttca gtgagctgtg ctgctgcttc tgtggccagt	1080
tcacgctctt ctgtattgaa agactcggaa tatggttggt tgaagattcc accaagatgt	1140

664674description (1)Sequence Listing

```

atgtttgata atccagatgc agataaaaca ctgaatcacc ttatatcggg gtttgaaaat 1200
tttgaaaaga aaatcaacta cagattcaag aataaggctt accttctcca ggcttttaca 1260
catgcctcct accactacaa tactatcact gattgttacc agcgcttaga attcctggga 1320
gatgcgattt tggactacct cataaccaag cacctttatg aagaccgcgc gcagcactcc 1380
ccgggggtcc tgacagacct gcggtctgcc ctggtcaaca acaccatctt tgcacgcgtg 1440
gctgtaaagt acgactacca caagtacttc aaagctgtct ctctgagct ottccatgtc 1500
attgatgact ttgtgcagtt tcagcttgag aagaatgaaa tgcaaggaat ggattctgag 1560
cttaggagat ctgaggagga tgaagagaaa gaagaggata ttgaagttcc aaaggccatg 1620
ggggatattt ttgagtcgct tgctgggtgcc atttaccatgg atagtgggat gtcactggag 1680
acagtctggc aggtgtacta tcccatgatg cggccactaa tagaaaagtt ttotgcaaatt 1740
gtaccccggt cccctgtgcg agaattgctt gaaatggaac cagaaactgc caaatttagc 1800
ccggctgaga gaacttacga cgggaaggtc agagtcactg tggaagtagt aggaaagggg 1860
aaatttaaag gtgttggtcg aagttacagg attgccaaat ctgcagcagc aagaagagcc 1920
ctccgaagcc tcaaagctaa tcaacctcag gttccaata gc 1962

```

<210> 4

<211> 654

<212> PRT

<213> Artificial sequence

<220>

<223> An amino acid sequence of human dicer mutant.

<400> 4

```

Gln Val Leu Lys Gly Arg Met Asp Ser Glu Gln Ser Pro Ser Ile Gly
1           5           10          15

```

```

Tyr Ser Ser Arg Thr Leu Gly Pro Asn Pro Gly Leu Ile Leu Gln Ala
          20          25          30

```

```

Leu Thr Leu Ser Asn Ala Ser Asp Gly Phe Asn Leu Glu Arg Leu Glu
          35          40          45

```

```

Met Leu Gly Asp Ser Phe Leu Lys His Ala Ile Thr Thr Tyr Leu Phe
          50          55          60

```

664674description (1)Sequence Listing
 Cys Thr Tyr Pro Asp Ala His Glu Gly Arg Leu Ser Tyr Met Arg Ser
 65 70 75 80

Lys Lys Val Ser Asn Cys Asn Leu Tyr Arg Leu Gly Lys Lys Lys Gly
 85 90 95

Leu Pro Ser Arg Met Val Val Ser Ile Phe Asp Pro Pro Val Asn Trp
 100 105 110

Leu Pro Pro Gly Tyr Val Val Asn Gln Asp Lys Ser Asn Thr Asp Lys
 115 120 125

Trp Glu Lys Asp Glu Met Thr Lys Asp Cys Met Leu Ala Asn Gly Lys
 130 135 140

Leu Asp Glu Asp Tyr Glu Glu Glu Asp Glu Glu Glu Glu Ser Leu Met
 145 150 155 160

Trp Arg Ala Pro Lys Glu Glu Ala Asp Tyr Glu Asp Asp Phe Leu Glu
 165 170 175

Tyr Asp Gln Glu His Ile Arg Phe Ile Asp Asn Met Leu Met Gly Ser
 180 185 190

Gly Ala Phe Val Lys Lys Ile Ser Leu Ser Pro Phe Ser Thr Thr Asp
 195 200 205

Ser Ala Tyr Glu Trp Lys Met Pro Lys Lys Ser Ser Leu Gly Ser Met
 210 215 220

Pro Phe Ser Ser Asp Phe Glu Asp Phe Asp Tyr Ser Ser Trp Asp Ala
 225 230 235 240

Met Cys Tyr Leu Asp Pro Ser Lys Ala Val Glu Glu Asp Asp Phe Val
 245 250 255

Val Gly Phe Trp Asn Pro Ser Glu Glu Asn Cys Gly Val Asp Thr Gly
 260 265 270

Lys Gln Ser Ile Ser Tyr Asp Leu His Thr Glu Gln Cys Ile Ala Asp
 275 280 285

664674description (1)Sequence Listing
 Lys Ser Ile Ala Asp Cys Val Glu Ala Leu Leu Gly Cys Tyr Leu Thr
 290 295 300

Ser Cys Gly Glu Arg Ala Ala Gln Leu Phe Leu Cys Ser Leu Gly Leu
 305 310 315 320

Lys Val Leu Pro Val Ile Lys Arg Thr Asp Arg Glu Lys Ala Leu Cys
 325 330 335

Pro Thr Arg Glu Asn Phe Asn Ser Gln Gln Lys Asn Leu Ser Val Ser
 340 345 350

Cys Ala Ala Ala Ser Val Ala Ser Ser Arg Ser Ser Val Leu Lys Asp
 355 360 365

Ser Glu Tyr Gly Cys Leu Lys Ile Pro Pro Arg Cys Met Phe Asp His
 370 375 380

Pro Asp Ala Asp Lys Thr Leu Asn His Leu Ile Ser Gly Phe Glu Asn
 385 390 395 400

Phe Glu Lys Lys Ile Asn Tyr Arg Phe Lys Asn Lys Ala Tyr Leu Leu
 405 410 415

Gln Ala Phe Thr His Ala Ser Tyr His Tyr Asn Thr Ile Thr Asp Cys
 420 425 430

Tyr Gln Arg Leu Glu Phe Leu Gly Asp Ala Ile Leu Asp Tyr Leu Ile
 435 440 445

Thr Lys His Leu Tyr Glu Asp Pro Arg Gln His Ser Pro Gly Val Leu
 450 455 460

Thr Asp Leu Arg Ser Ala Leu Val Asn Asn Thr Ile Phe Ala Ser Leu
 465 470 475 480

Ala Val Lys Tyr Asp Tyr His Lys Tyr Phe Lys Ala Val Ser Pro Glu
 485 490 495

Leu Phe His Val Ile Asp Asp Phe Val Gln Phe Gln Leu Glu Lys Asn
 500 505 510

664674description (1)Sequence Listing

Glu Met Gln Gly Met Asp Ser Glu Leu Arg Arg Ser Glu Glu Asp Glu
515 520 525

Glu Lys Glu Glu Asp Ile Glu Val Pro Lys Ala Met Gly Asp Ile Phe
530 535 540

Glu Ser Leu Ala Gly Ala Ile Tyr Met Asp Ser Gly Met Ser Leu Glu
545 550 555 560

Thr Val Trp Gln Val Tyr Tyr Pro Met Met Arg Pro Leu Ile Glu Lys
565 570 575

Phe Ser Ala Asn Val Pro Arg Ser Pro Val Arg Glu Leu Leu Glu Met
580 585 590

Glu Pro Glu Thr Ala Lys Phe Ser Pro Ala Glu Arg Thr Tyr Asp Gly
595 600 605

Lys Val Arg Val Thr Val Glu Val Val Gly Lys Gly Lys Phe Lys Gly
610 615 620

Val Gly Arg Ser Tyr Arg Ile Ala Lys Ser Ala Ala Ala Arg Arg Ala
625 630 635 640

Leu Arg Ser Leu Lys Ala Asn Gln Pro Gln Val Pro Asn Ser
645 650

<210> 5

<211> 36

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic primer 1 to amplify a gene encoding human dicer

<400> 5

tcgagctcgg taccccaagt gctcaagggc aggatg

36

<210> 6

<211> 36

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic primer 2 to amplify a gene encoding human dicer

664674description (1)Sequence Listing

<400> 6
tatctagaaa gcttttagct attggaacc tgaggt 36

<210> 7
<211> 42
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer 3 to amplify a gene encoding red-shifted green fluorescence protein

<400> 7
gggtaatacg actcactata gggagaatgg ctagcaaagg ag 42

<210> 8
<211> 42
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic primer 4 to amplify a gene encoding red-shifted green fluorescence protein

<400> 8
gggtaatacg actcactata gggagatcag ttgtacagtt ca 42

<210> 9
<211> 66
<212> PRT
<213> Thermotoga maritima

<400> 9

Met Arg Gly Lys Val Lys Trp Phe Asp Ser Lys Lys Gly Tyr Gly Phe
1 5 10 15

Ile Thr Lys Asp Glu Gly Gly Asp Val Phe Val His Trp Ser Ala Ile
20 25 30

Glu Met Glu Gly Phe Lys Thr Leu Lys Glu Gly Gln Val Val Glu Phe
35 40 45

Glu Ile Gln Glu Gly Lys Lys Gly Pro Gln Ala Ala His Val Lys Val
50 55 60

Val Glu
65

664674description (1)Sequence Listing

<210> 10
 <211> 198
 <212> DNA
 <213> Thermotoga maritima

<400> 10
 atgagaggaa aggttaagtg gttcgattcc aagaagggt acggattcat cacaaaggac 60
 gaaggaggag acgtgttcgt aacttggtca gccatcgaaa tggaagggtt caaaactctg 120
 aaggaaggcc aggtogtoga gttcgagatt caggaaggca agaaagggtcc acaggcagcg 180
 cacgtgaaag tagttgag 198

<210> 11
 <211> 720
 <212> DNA
 <213> Artificial sequence

<220>
 <223> A gene encoding red-shifted green fluorescence protein.

<400> 11
 atggctagca aaggagaaga actcttcact ggagttgtcc caattcttgt tgaattagat 60
 ggtgatgtta acggccacaa gttctctgtc agtggagagg gtgaaggatga tgcaacatac 120
 ggaaaactta cccatgaagt catctgcact actggcaaac tgctgtttcc atggccaaca 180
 ctagtcaacta ctctgtgcta tgggtgttcaa tgcttttcaa gatacccgga tcatatgaaa 240
 cggcatgact ttttcaagag tgccatgccc gaaggttatg tacaggaaag gaccatcttc 300
 ttcaaagatg acggcaacta caagacacgt gctgaagtca agtttgaagg tgataccott 360
 gttaatagaa tcgagttaaa aggtattgac ttcaaggaag atggaaacat totgggacac 420
 aaattggaat acaactataa ctacacacat gtatacatca tggcagacaa acaaaagaat 480
 ggaatcaaag tgaacttcaa gacccgccac aacattgaag atggaagcgt tcaactagca 540
 gaccattatc aacaaaatac tccaattggc gatggccctg tccttttacc agacaacat 600
 tacctgtcca cacaatctgc cttttcgaaa gatcccaacg aaaagagaga ccacatggtc 660
 ottottgagt ttgtaacagc tgctgggatt acacatggca tggatgaact gtacaactga 720

<210> 12
 <211> 675
 <212> PRT
 <213> Artificial sequence

<220>

664674description (1)Sequence Listing

<223> An amino acid sequence of human dicer mutant

<400> 12

Met Asn His Lys Val His His His His His His Ile Glu Gly Arg Asn
1 5 10 15

Ser Ser Ser Val Pro Gln Val Leu Lys Gly Arg Met Asp Ser Glu Gln
20 25 30

Ser Pro Ser Ile Gly Tyr Ser Ser Arg Thr Leu Gly Pro Asn Pro Gly
35 40 45

Leu Ile Leu Gln Ala Leu Thr Leu Ser Asn Ala Ser Asp Gly Phe Asn
50 55 60

Leu Glu Arg Leu Glu Met Leu Gly Asp Ser Phe Leu Lys His Ala Ile
65 70 75 80

Thr Thr Tyr Leu Phe Cys Thr Tyr Pro Asp Ala His Glu Gly Arg Leu
85 90 95

Ser Tyr Met Arg Ser Lys Lys Val Ser Asn Cys Asn Leu Tyr Arg Leu
100 105 110

Gly Lys Lys Lys Gly Leu Pro Ser Arg Met Val Val Ser Ile Phe Asp
115 120 125

Pro Pro Val Asn Trp Leu Pro Pro Gly Tyr Val Val Asn Gln Asp Lys
130 135 140

Ser Asn Thr Asp Lys Trp Glu Lys Asp Glu Met Thr Lys Asp Cys Met
145 150 155 160

Leu Ala Asn Gly Lys Leu Asp Glu Asp Tyr Glu Glu Glu Asp Glu Glu
165 170 175

Glu Glu Ser Leu Met Trp Arg Ala Pro Lys Glu Glu Ala Asp Tyr Glu
180 185 190

Asp Asp Phe Leu Glu Tyr Asp Gln Glu His Ile Arg Phe Ile Asp Asn
195 200 205

664674description (1)Sequence Listing

Met Leu Met Gly Ser Gly Ala Phe Val Lys Lys Ile Ser Leu Ser Pro
 210 215 220

Phe Ser Thr Thr Asp Ser Ala Tyr Glu Trp Lys Met Pro Lys Lys Ser
 225 230 235 240

Ser Leu Gly Ser Met Pro Phe Ser Ser Asp Phe Glu Asp Phe Asp Tyr
 245 250 255

Ser Ser Trp Asp Ala Met Cys Tyr Leu Asp Pro Ser Lys Ala Val Glu
 260 265 270

Glu Asp Asp Phe Val Val Gly Phe Trp Asn Pro Ser Glu Glu Asn Cys
 275 280 285

Gly Val Asp Thr Gly Lys Gln Ser Ile Ser Tyr Asp Leu His Thr Glu
 290 295 300

Gln Cys Ile Ala Asp Lys Ser Ile Ala Asp Cys Val Glu Ala Leu Leu
 305 310 315 320

Gly Cys Tyr Leu Thr Ser Cys Gly Glu Arg Ala Ala Gln Leu Phe Leu
 325 330 335

Cys Ser Leu Gly Leu Lys Val Leu Pro Val Ile Lys Arg Thr Asp Arg
 340 345 350

Glu Lys Ala Leu Cys Pro Thr Arg Glu Asn Phe Asn Ser Gln Gln Lys
 355 360 365

Asn Leu Ser Val Ser Cys Ala Ala Ala Ser Val Ala Ser Ser Arg Ser
 370 375 380

Ser Val Leu Lys Asp Ser Glu Tyr Gly Cys Leu Lys Ile Pro Pro Arg
 385 390 395 400

Cys Met Phe Asp His Pro Asp Ala Asp Lys Thr Leu Asn His Leu Ile
 405 410 415

Ser Gly Phe Glu Asn Phe Glu Lys Lys Ile Asn Tyr Arg Phe Lys Asn
 420 425 430

664674description (1)Sequence Listing

Lys Ala Tyr Leu Leu Gln Ala Phe Thr His Ala Ser Tyr His Tyr Asn
 435 440 445
 Thr Ile Thr Asp Cys Tyr Gln Arg Leu Glu Phe Leu Gly Asp Ala Ile
 450 455 460
 Leu Asp Tyr Leu Ile Thr Lys His Leu Tyr Glu Asp Pro Arg Gln His
 465 470 475 480
 Ser Pro Gly Val Leu Thr Asp Leu Arg Ser Ala Leu Val Asn Asn Thr
 485 490 495
 Ile Phe Ala Ser Leu Ala Val Lys Tyr Asp Tyr His Lys Tyr Phe Lys
 500 505 510
 Ala Val Ser Pro Glu Leu Phe His Val Ile Asp Asp Phe Val Gln Phe
 515 520 525
 Gln Leu Glu Lys Asn Glu Met Gln Gly Met Asp Ser Glu Leu Arg Arg
 530 535 540
 Ser Glu Glu Asp Glu Glu Lys Glu Glu Asp Ile Glu Val Pro Lys Ala
 545 550 555 560
 Met Gly Asp Ile Phe Glu Ser Leu Ala Gly Ala Ile Tyr Met Asp Ser
 565 570 575
 Gly Met Ser Leu Glu Thr Val Trp Gln Val Tyr Tyr Pro Met Met Arg
 580 585 590
 Pro Leu Ile Glu Lys Phe Ser Ala Asn Val Pro Arg Ser Pro Val Arg
 595 600 605
 Glu Leu Leu Glu Met Glu Pro Glu Thr Ala Lys Phe Ser Pro Ala Glu
 610 615 620
 Arg Thr Tyr Asp Gly Lys Val Arg Val Thr Val Glu Val Val Gly Lys
 625 630 635 640
 Gly Lys Phe Lys Gly Val Gly Arg Ser Tyr Arg Ile Ala Lys Ser Ala
 645 650 655

664674description (1)Sequence Listing

Ala Ala Arg Arg Ala Leu Arg Ser Leu Lys Ala Asn Gln Pro Gln Val
 660 665 670

Pro Asn Ser
 675

<210> 13
 <211> 2025
 <212> DNA
 <213> Artificial sequence

<220>
 <223> A gene encoding human dicer mutant

<400> 13
 atgaatcaca aagtgcacatc tcatcatcat catatcgaag gtaggaattc gagctcggta 60
 ccccaagtgc tcaagggcag gatggattct gagcagagcc cttctattgg gtactcctca 120
 aggactcttg gcccacatcc tggacttatt cttcaggctt tgactctgtc aaacgctagt 180
 gatggattta acctggagcg gcttgaaatg cttggcgact cttttttaaa gcatgccatc 240
 accacatatc ttttttgac ttacctgat gcgcatgagg gccgcctttc atatatgaga 300
 agcaaaaagg tcagcaactg taatctgtat cgccttgga aaaagaaggg actaccagc 360
 ogcatgggtg tgtcaatatt tgatccccct gtgaattggc ttctctctgg ttatgtagta 420
 aatcaagaca aaagcaacac agataaatgg gaaaaagatg aaatgacaaa agactgcatg 480
 ctggcgaatg gcaaaactgga tgaggattac gaggaggagg atgaggagga ggagagcctg 540
 atgtggaggg ctccgaagga agaggctgac tatgaagatg atttcctgga gtatgatcag 600
 gaacatatca gatttataga taatatgtta atggggtcag gagcttttgt aaagaaaatc 660
 totctttctc ctttttcaac cactgattct gcatatgaat ggaaaatgcc caaaaaatcc 720
 tccttaggta gtatgccatt ttcacagat tttaggatt ttgactacag ctcttgggat 780
 gcaatgtgct atctggatcc tagcaaagct gttgaagaag atgactttgt ggtgggggtc 840
 tggaatccat cagaagaaaa ctgtggtgtt gacacgggaa agcagtccat ttcttacgac 900
 ttgcacactg agcagtgtat tgctgacaaa agcatagcgg actgtgtgga agccctgctg 960
 ggctgctatt taaccagctg tggggagagg gctgctcagc ttttcctctg ttactgggg 1020
 ctgaaggtgc tcccggtaat taaaaggact gatcgggaaa aggccctgtg ccctactcgg 1080
 gagaatttca acagccaaca aaagaacctt tcagttagct gtgctgctgc ttctgtggcc 1140

664674description (1)Sequence Listing

```

agttcacgct cttctgtatt gaaagactcg gaatatgggt gtttgaagat tccaccaaga 1200
tgtatgtttg atcatccaga tgcagataaa aactgaatc accttatatc ggggtttgaa 1260
aattttgaaa agaaaatcaa ctacagattc aagaataagg cttaccttct ccaggctttt 1320
acacatgcct cctaccacta caatactatc actgattgtt accagcgctt agaattcctg 1380
ggagatgcga ttttgacta cctcataaacc aagcaccttt atgaagaccc gcggcagcac 1440
tccccggggg tcctgacaga cctgcggtct gccctgggtca acaacaccat ctttgcacg 1500
ctggctgtaa agtacgacta ccacaagtac ttcaaagctg totctcctga gctcttccat 1560
gtcattgatg actttgtgca gtttcagott gagaagaatg aaatgcaagg aatggattct 1620
gagcttagga gatctgagga ggatgaagag aaagaagagg atattgaagt tccaaaggcc 1680
atgggggata tttttgagtc gcttgctggt gccatttaca tggatagtgg gatgtcactg 1740
gagacagtct ggcagggtga ctatcccatg atgcggccac taatagaaaa gttttctgca 1800
aatgtacccc gttcccctgt gcgagaattg cttgaaatgg aaccagaaac tgccaaattt 1860
agcccggctg agagaactta cgacgggaag gtcagagtca ctgtggaagt agtaggaaag 1920
gggaaattta aagggtgttg togaagttac aggattgcca aatctgcagc agcaagaaga 1980
gccctccgaa gcctcaaagc taatcaacct caggttccca atagc 2025

```

<210> 14
 <211> 36
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic primer 5 to amplify a gene encoding human dicer mutant

<400> 14
 tcgagctcgg taccgcctc cattgttggt ccacca 36

<210> 15
 <211> 36
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic primer 6 to amplify a gene encoding human dicer mutant

<400> 15
 tatctagaaa gcttttagct attgggaacc tgagg 36

<210> 16
 <211> 3741

664674description (1)Sequence Listing

<212> DNA
 <213> Artificial

<220>
 <223> A gene encoding human dicer mutant

<400> 16
 gcctccattg ttggtccacc aatgagctgt gtacgattgg ctgaaagagt tgtcgctctc 60
 atttgcctgtg agaaactgca caaaattggc gaactggatg accatttgat gccagttggg 120
 aaagagactg ttaaataatga agaggagctt gatttgcatt atgaagaaga gaccagtggt 180
 ccaggaagac caggttccac gaaacgaagg cagtgtctacc caaaagcaat tccagagtgt 240
 ttgagggata gttatcccag acctgatcag ccctgttacc tgtatgtgat aggaatgggt 300
 ttaactacac ctttacctga tgaactcaac tttagaaggc ggaagctcta tcctcctgaa 360
 gataccacaa gatgcttttg aatactgacg gccaaacca tacctcagat tccacacttt 420
 cctgtgtaca cagctcttg agaggttacc atatccattg agttgaagaa gtctggtttc 480
 atgttgtctc tacaaatgct tgagttgatt acaagacttc accagtatat attctcacat 540
 attcttcggc ttgaaaaacc tgcactagaa tttaaacctc cagacgctga ttcagcatac 600
 tgtgtttctac ctottaatgt tgtaaatgac tccagcactt tggatattga ctttaaattc 660
 atggaagata ttgagaagtc tgaagctcgc ataggcattc ccagtacaaa gtatacaaaa 720
 gaaacaccct ttgtttttta attagaagat taccaagatg ccgttatcat tccaagatat 780
 cgcaattttg atcagcctca tcgattttat gtagctgatg tgtacactga tottaccoca 840
 ctocagtaa at ttocctcccc tgagtatgaa acttttgcag aatattataa aacaaagtac 900
 aaccttgacc taaccaatct caaccagcca ctgctggatg tggaccacac atcttcaaga 960
 cttaatcttt tgacacctcg acatttgaat cagaagggga aagcgcttc ttttaagcagt 1020
 gctgagaaga ggaaagccaa atgggaaagt ctgcagaata aacagatact ggttccagaa 1080
 ctotgtgota tacatccaat tccagcatca ctgtggagaa aagctgtttg tctccccagc 1140
 atactttatc gccttcaactg ctttttgact gcagaggagc taagagccca gactgccagc 1200
 gatgctggcg tgggagtcag atcacttctt goggatttta gataccctaa cttagacttc 1260
 ggggtggaaaa aatctattga cagcaaactt ttcatctcaa tttotaactc ctcttcagct 1320
 gaaaatgata attactgtaa gcacagcaca attgtccctg aaaatgctgc acatcaaggt 1380
 gctaatagaa cctcctctct agaaaatcat gaccaaagt ctgtgaactg cagaacgttg 1440
 ctocagcagc cccctggtaa gctccacgtt gaagtttcag cagatcttac agcaattaat 1500

664674description (1)Sequence Listing

ggtcttttctt acaatcaaaa totcgccaat ggcagttatg atttagctaa cagagacttt	1560
tgccaaggaa atcagctaaa ttactacaag caggaaatac ccgtgcaacc aactacctca	1620
tattccattc agaatttata cagttacgag aaccagcccc agcccagcga tgaatgtact	1680
ctcctgagta ataaatacct tgatggaaat gctaacaaat ctacctcaga tggaagtcct	1740
gtgatggcog taatgcctgg tacgacagac actattcaag tgctcaaggg caggatggat	1800
tctgagcaga gcccttttat tgggtactcc tcaaggactc ttggcccaa toctggactt	1860
attcttcagg ctttgactct gtcaaacgct agtgatggat ttaacctgga ggggcttgaa	1920
atgcttggcg actccttttt aaagcatgcc atcaccacat atctattttg cacttaccct	1980
gatgcgcattg agggccgcct ttcatatatg agaagcaaaa aggtcagcaa ctgtaatctg	2040
tatgccttg gaaaaaagaa gggactaccc agccgcattg tgggtgcaat atttgatccc	2100
cctgtgaatt ggcttcctcc tggttatgta gtaaatacaag acaaaagcaa cacagataaa	2160
tgggaaaaag atgaaatgac aaaagactgc atgctggcga atggcaaact ggatgaggat	2220
tacgaggagg aggatgagga ggaggagagc ctgatgtgga gggctccgaa ggaagaggct	2280
gactatgaag atgatttcct ggagtatgat caggaacata tcagatttat agataatatg	2340
ttaatggggt caggagcttt tgtaaagaaa atctctcttt ctctttttc aaccactgat	2400
tctgcatatg aatggaaaat gcccaaaaaa tcctccttag gtagtatgcc attttcatca	2460
gattttgagg attttgacta cagctcttgg gatgcaatgt gctatctgga tcctagcaaa	2520
gctgttgaag aagatgactt tgttggtgggg ttctggaatc catcagaaga aaactgtggt	2580
gttgacacgg gaaagcagtc catttcttac gacttgcaca ctgagcagtg tattgctgac	2640
aaaagcatag cggactgtgt ggaagccctg ctgggctgct atttaaccag ctgtggggag	2700
agggotgctc agcttttcct ctgttcactg gggctgaagg tgctcccgtt aattaaaagg	2760
actgatcggg aaaaggccct gtgccctact cgggagaatt tcaacagcca acaaaagaac	2820
ctttcagtga gctgtgctgc tgcttctgtg gccagttcac gctcttctgt attgaaagac	2880
toggaatatg gttgtttgaa gattccacca agatgtatgt ttgatcatcc agatgcagat	2940
aaaacactga atcaccttat atcgggggtt gaaaattttg aaaagaaaat caactacaga	3000
ttcaagaata aggcttacct tctccaggct tttaacatg cctcctacca ctacaatact	3060
atcactgatt gttaccagcg cttagaattc ctgggagatg cgattttgga ctacctcata	3120
accaagcacc tttatgaaga cccgcggcag cactccccgg gggctcctgac agacctgcgg	3180

664674description (1)Sequence Listing

```
tctgccctgg tcaacaacac catcttttga tcgctggctg taaagtacga ctaccacaag 3240
tacttcaaag ctgtctctcc tgagctcttc catgtcattg atgactttgt gcagtttcag 3300
cttgagaaga atgaaatgca aggaatggat tctgagctta ggagatctga ggaggatgaa 3360
gagaaagaag aggatattga agttccaaag gccatggggg atatTTTTga gtcgcttgct 3420
ggtgccattt acatggatag tgggatgtca ctggagacag tctggcaggt gtactatccc 3480
atgatgcggc cactaataga aaagttttct gcaaagtac cccgttcccc tgtgcgagaa 3540
ttgcttgaag tggaaccaga aactgccaaa tttagcccg gctgagagaac ttacgacggg 3600
aaggtcagag tcaactgtga agtagtagga aaggggaaat ttaaaggtgt tggtcgaagt 3660
tacaggattg ccaaattctgc agcagcaaga agagccctcc gaagcctcaa agctaataa 3720
cctcaggttc ccaatagcta a 3741
```

<210> 17
 <211> 1246
 <212> PRT
 <213> Artificial

<220>
 <223> An amino acid sequence of human dicer mutant

<400> 17

```
Ala Ser Ile Val Gly Pro Pro Met Ser Cys Val Arg Leu Ala Glu Arg
1          5          10          15
```

```
Val Val Ala Leu Ile Cys Cys Glu Lys Leu His Lys Ile Gly Glu Leu
20          25          30
```

```
Asp Asp His Leu Met Pro Val Gly Lys Glu Thr Val Lys Tyr Glu Glu
35          40          45
```

```
Glu Leu Asp Leu His Asp Glu Glu Glu Thr Ser Val Pro Gly Arg Pro
50          55          60
```

```
Gly Ser Thr Lys Arg Arg Gln Cys Tyr Pro Lys Ala Ile Pro Glu Cys
65          70          75          80
```

```
Leu Arg Asp Ser Tyr Pro Arg Pro Asp Gln Pro Cys Tyr Leu Tyr Val
85          90          95
```

664674description (1)Sequence Listing

Ile Gly Met Val Leu Thr Thr Pro Leu Pro Asp Glu Leu Asn Phe Arg
 100 105 110
 Arg Arg Lys Leu Tyr Pro Pro Glu Asp Thr Thr Arg Cys Phe Gly Ile
 115 120 125
 Leu Thr Ala Lys Pro Ile Pro Gln Ile Pro His Phe Pro Val Tyr Thr
 130 135 140
 Arg Ser Gly Glu Val Thr Ile Ser Ile Glu Leu Lys Lys Ser Gly Phe
 145 150 155 160
 Met Leu Ser Leu Gln Met Leu Glu Leu Ile Thr Arg Leu His Gln Tyr
 165 170 175
 Ile Phe Ser His Ile Leu Arg Leu Glu Lys Pro Ala Leu Glu Phe Lys
 180 185 190
 Pro Thr Asp Ala Asp Ser Ala Tyr Cys Val Leu Pro Leu Asn Val Val
 195 200 205
 Asn Asp Ser Ser Thr Leu Asp Ile Asp Phe Lys Phe Met Glu Asp Ile
 210 215 220
 Glu Lys Ser Glu Ala Arg Ile Gly Ile Pro Ser Thr Lys Tyr Thr Lys
 225 230 235 240
 Glu Thr Pro Phe Val Phe Lys Leu Glu Asp Tyr Gln Asp Ala Val Ile
 245 250 255
 Ile Pro Arg Tyr Arg Asn Phe Asp Gln Pro His Arg Phe Tyr Val Ala
 260 265 270
 Asp Val Tyr Thr Asp Leu Thr Pro Leu Ser Lys Phe Pro Ser Pro Glu
 275 280 285
 Tyr Glu Thr Phe Ala Glu Tyr Tyr Lys Thr Lys Tyr Asn Leu Asp Leu
 290 295 300
 Thr Asn Leu Asn Gln Pro Leu Leu Asp Val Asp His Thr Ser Ser Arg
 305 310 315 320

664674description (1)Sequence Listing

Leu Asn Leu Leu Thr Pro Arg His Leu Asn Gln Lys Gly Lys Ala Leu
325 330 335

Pro Leu Ser Ser Ala Glu Lys Arg Lys Ala Lys Trp Glu Ser Leu Gln
340 345 350

Asn Lys Gln Ile Leu Val Pro Glu Leu Cys Ala Ile His Pro Ile Pro
355 360 365

Ala Ser Leu Trp Arg Lys Ala Val Cys Leu Pro Ser Ile Leu Tyr Arg
370 375 380

Leu His Cys Leu Leu Thr Ala Glu Glu Leu Arg Ala Gln Thr Ala Ser
385 390 395 400

Asp Ala Gly Val Gly Val Arg Ser Leu Pro Ala Asp Phe Arg Tyr Pro
405 410 415

Asn Leu Asp Phe Gly Trp Lys Lys Ser Ile Asp Ser Lys Ser Phe Ile
420 425 430

Ser Ile Ser Asn Ser Ser Ser Ala Glu Asn Asp Asn Tyr Cys Lys His
435 440 445

Ser Thr Ile Val Pro Glu Asn Ala Ala His Gln Gly Ala Asn Arg Thr
450 455 460

Ser Ser Leu Glu Asn His Asp Gln Met Ser Val Asn Cys Arg Thr Leu
465 470 475 480

Leu Ser Glu Ser Pro Gly Lys Leu His Val Glu Val Ser Ala Asp Leu
485 490 495

Thr Ala Ile Asn Gly Leu Ser Tyr Asn Gln Asn Leu Ala Asn Gly Ser
500 505 510

Tyr Asp Leu Ala Asn Arg Asp Phe Cys Gln Gly Asn Gln Leu Asn Tyr
515 520 525

Tyr Lys Gln Glu Ile Pro Val Gln Pro Thr Thr Ser Tyr Ser Ile Gln
530 535 540

664674description (1)Sequence Listing

Asn	Leu	Tyr	Ser	Tyr	Glu	Asn	Gln	Pro	Gln	Pro	Ser	Asp	Glu	Cys	Thr
545					550					555					560
Leu	Leu	Ser	Asn	Lys	Tyr	Leu	Asp	Gly	Asn	Ala	Asn	Lys	Ser	Thr	Ser
				565					570					575	
Asp	Gly	Ser	Pro	Val	Met	Ala	Val	Met	Pro	Gly	Thr	Thr	Asp	Thr	Ile
			580					585					590		
Gln	Val	Leu	Lys	Gly	Arg	Met	Asp	Ser	Glu	Gln	Ser	Pro	Ser	Ile	Gly
		595					600					605			
Tyr	Ser	Ser	Arg	Thr	Leu	Gly	Pro	Asn	Pro	Gly	Leu	Ile	Leu	Gln	Ala
	610					615					620				
Leu	Thr	Leu	Ser	Asn	Ala	Ser	Asp	Gly	Phe	Asn	Leu	Glu	Arg	Leu	Glu
625					630					635					640
Met	Leu	Gly	Asp	Ser	Phe	Leu	Lys	His	Ala	Ile	Thr	Thr	Tyr	Leu	Phe
				645					650					655	
Cys	Thr	Tyr	Pro	Asp	Ala	His	Glu	Gly	Arg	Leu	Ser	Tyr	Met	Arg	Ser
			660					665					670		
Lys	Lys	Val	Ser	Asn	Cys	Asn	Leu	Tyr	Arg	Leu	Gly	Lys	Lys	Lys	Gly
		675					680					685			
Leu	Pro	Ser	Arg	Met	Val	Val	Ser	Ile	Phe	Asp	Pro	Pro	Val	Asn	Trp
	690					695					700				
Leu	Pro	Pro	Gly	Tyr	Val	Val	Asn	Gln	Asp	Lys	Ser	Asn	Thr	Asp	Lys
705					710					715					720
Trp	Glu	Lys	Asp	Glu	Met	Thr	Lys	Asp	Cys	Met	Leu	Ala	Asn	Gly	Lys
				725					730					735	
Leu	Asp	Glu	Asp	Tyr	Glu	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Ser	Leu	Met
			740					745					750		
Trp	Arg	Ala	Pro	Lys	Glu	Glu	Ala	Asp	Tyr	Glu	Asp	Asp	Phe	Leu	Glu
		755					760					765			

664674description (1)Sequence Listing

Tyr Asp Gln Glu His Ile Arg Phe Ile Asp Asn Met Leu Met Gly Ser
 770 775 780

Gly Ala Phe Val Lys Lys Ile Ser Leu Ser Pro Phe Ser Thr Thr Asp
 785 790 795 800

Ser Ala Tyr Glu Trp Lys Met Pro Lys Lys Ser Ser Leu Gly Ser Met
 805 810 815

Pro Phe Ser Ser Asp Phe Glu Asp Phe Asp Tyr Ser Ser Trp Asp Ala
 820 825 830

Met Cys Tyr Leu Asp Pro Ser Lys Ala Val Glu Glu Asp Asp Phe Val
 835 840 845

Val Gly Phe Trp Asn Pro Ser Glu Glu Asn Cys Gly Val Asp Thr Gly
 850 855 860

Lys Gln Ser Ile Ser Tyr Asp Leu His Thr Glu Gln Cys Ile Ala Asp
 865 870 875 880

Lys Ser Ile Ala Asp Cys Val Glu Ala Leu Leu Gly Cys Tyr Leu Thr
 885 890 895

Ser Cys Gly Glu Arg Ala Ala Gln Leu Phe Leu Cys Ser Leu Gly Leu
 900 905 910

Lys Val Leu Pro Val Ile Lys Arg Thr Asp Arg Glu Lys Ala Leu Cys
 915 920 925

Pro Thr Arg Glu Asn Phe Asn Ser Gln Gln Lys Asn Leu Ser Val Ser
 930 935 940

Cys Ala Ala Ala Ser Val Ala Ser Ser Arg Ser Ser Val Leu Lys Asp
 945 950 955 960

Ser Glu Tyr Gly Cys Leu Lys Ile Pro Pro Arg Cys Met Phe Asp His
 965 970 975

Pro Asp Ala Asp Lys Thr Leu Asn His Leu Ile Ser Gly Phe Glu Asn
 980 985 990

664674description (1)Sequence Listing

Phe Glu Lys Lys Ile Asn Tyr Arg Phe Lys Asn Lys Ala Tyr Leu Leu
 995 1000 1005

Gln Ala Phe Thr His Ala Ser Tyr His Tyr Asn Thr Ile Thr Asp
 1010 1015 1020

Cys Tyr Gln Arg Leu Glu Phe Leu Gly Asp Ala Ile Leu Asp Tyr
 1025 1030 1035

Leu Ile Thr Lys His Leu Tyr Glu Asp Pro Arg Gln His Ser Pro
 1040 1045 1050

Gly Val Leu Thr Asp Leu Arg Ser Ala Leu Val Asn Asn Thr Ile
 1055 1060 1065

Phe Ala Ser Leu Ala Val Lys Tyr Asp Tyr His Lys Tyr Phe Lys
 1070 1075 1080

Ala Val Ser Pro Glu Leu Phe His Val Ile Asp Asp Phe Val Gln
 1085 1090 1095

Phe Gln Leu Glu Lys Asn Glu Met Gln Gly Met Asp Ser Glu Leu
 1100 1105 1110

Arg Arg Ser Glu Glu Asp Glu Glu Lys Glu Glu Asp Ile Glu Val
 1115 1120 1125

Pro Lys Ala Met Gly Asp Ile Phe Glu Ser Leu Ala Gly Ala Ile
 1130 1135 1140

Tyr Met Asp Ser Gly Met Ser Leu Glu Thr Val Trp Gln Val Tyr
 1145 1150 1155

Tyr Pro Met Met Arg Pro Leu Ile Glu Lys Phe Ser Ala Asn Val
 1160 1165 1170

Pro Arg Ser Pro Val Arg Glu Leu Leu Glu Met Glu Pro Glu Thr
 1175 1180 1185

Ala Lys Phe Ser Pro Ala Glu Arg Thr Tyr Asp Gly Lys Val Arg
 1190 1195 1200

664674description (1)Sequence Listing

Val Thr Val Glu Val Val Gly Lys Gly Lys Phe Lys Gly Val Gly
1205 1210 1215

Arg Ser Tyr Arg Ile Ala Lys Ser Ala Ala Ala Arg Arg Ala Leu
1220 1225 1230

Arg Ser Leu Lys Ala Asn Gln Pro Gln Val Pro Asn Ser
1235 1240 1245

<210> 18
<211> 1267
<212> PRT
<213> Artificial

<220>
<223> An amino acid sequence of human dicer mutant

<400> 18

Met Asn His Lys Val His His His His His His Ile Glu Gly Arg Asn
1 5 10 15

Ser Ser Ser Val Pro Ala Ser Ile Val Gly Pro Pro Met Ser Cys Val
20 25 30

Arg Leu Ala Glu Arg Val Val Ala Leu Ile Cys Cys Glu Lys Leu His
35 40 45

Lys Ile Gly Glu Leu Asp Asp His Leu Met Pro Val Gly Lys Glu Thr
50 55 60

Val Lys Tyr Glu Glu Glu Leu Asp Leu His Asp Glu Glu Glu Thr Ser
65 70 75 80

Val Pro Gly Arg Pro Gly Ser Thr Lys Arg Arg Gln Cys Tyr Pro Lys
85 90 95

Ala Ile Pro Glu Cys Leu Arg Asp Ser Tyr Pro Arg Pro Asp Gln Pro
100 105 110

Cys Tyr Leu Tyr Val Ile Gly Met Val Leu Thr Thr Pro Leu Pro Asp
115 120 125

Glu Leu Asn Phe Arg Arg Arg Lys Leu Tyr Pro Pro Glu Asp Thr Thr
ページ (34)

664674description (1)Sequence Listing

130

135

140

Arg Cys Phe Gly Ile Leu Thr Ala Lys Pro Ile Pro Gln Ile Pro His
145 150 155 160

Phe Pro Val Tyr Thr Arg Ser Gly Glu Val Thr Ile Ser Ile Glu Leu
165 170 175

Lys Lys Ser Gly Phe Met Leu Ser Leu Gln Met Leu Glu Leu Ile Thr
180 185 190

Arg Leu His Gln Tyr Ile Phe Ser His Ile Leu Arg Leu Glu Lys Pro
195 200 205

Ala Leu Glu Phe Lys Pro Thr Asp Ala Asp Ser Ala Tyr Cys Val Leu
210 215 220

Pro Leu Asn Val Val Asn Asp Ser Ser Thr Leu Asp Ile Asp Phe Lys
225 230 235 240

Phe Met Glu Asp Ile Glu Lys Ser Glu Ala Arg Ile Gly Ile Pro Ser
245 250 255

Thr Lys Tyr Thr Lys Glu Thr Pro Phe Val Phe Lys Leu Glu Asp Tyr
260 265 270

Gln Asp Ala Val Ile Ile Pro Arg Tyr Arg Asn Phe Asp Gln Pro His
275 280 285

Arg Phe Tyr Val Ala Asp Val Tyr Thr Asp Leu Thr Pro Leu Ser Lys
290 295 300

Phe Pro Ser Pro Glu Tyr Glu Thr Phe Ala Glu Tyr Tyr Lys Thr Lys
305 310 315 320

Tyr Asn Leu Asp Leu Thr Asn Leu Asn Gln Pro Leu Leu Asp Val Asp
325 330 335

His Thr Ser Ser Arg Leu Asn Leu Leu Thr Pro Arg His Leu Asn Gln
340 345 350

Lys Gly Lys Ala Leu Pro Leu Ser Ser Ala Glu Lys Arg Lys Ala Lys
ページ (35)

664674description (1)Sequence Listing

355
 Trp Glu Ser Leu Gln Asn Lys Gln Ile Leu Val Pro Glu Leu Cys Ala
 370 375 380
 Ile His Pro Ile Pro Ala Ser Leu Trp Arg Lys Ala Val Cys Leu Pro
 385 390 395 400
 Ser Ile Leu Tyr Arg Leu His Cys Leu Leu Thr Ala Glu Glu Leu Arg
 405 410 415
 Ala Gln Thr Ala Ser Asp Ala Gly Val Gly Val Arg Ser Leu Pro Ala
 420 425 430
 Asp Phe Arg Tyr Pro Asn Leu Asp Phe Gly Trp Lys Lys Ser Ile Asp
 435 440 445
 Ser Lys Ser Phe Ile Ser Ile Ser Asn Ser Ser Ser Ala Glu Asn Asp
 450 455 460
 Asn Tyr Cys Lys His Ser Thr Ile Val Pro Glu Asn Ala Ala His Gln
 465 470 475 480
 Gly Ala Asn Arg Thr Ser Ser Leu Glu Asn His Asp Gln Met Ser Val
 485 490 495
 Asn Cys Arg Thr Leu Leu Ser Glu Ser Pro Gly Lys Leu His Val Glu
 500 505 510
 Val Ser Ala Asp Leu Thr Ala Ile Asn Gly Leu Ser Tyr Asn Gln Asn
 515 520 525
 Leu Ala Asn Gly Ser Tyr Asp Leu Ala Asn Arg Asp Phe Cys Gln Gly
 530 535 540
 Asn Gln Leu Asn Tyr Tyr Lys Gln Glu Ile Pro Val Gln Pro Thr Thr
 545 550 555 560
 Ser Tyr Ser Ile Gln Asn Leu Tyr Ser Tyr Glu Asn Gln Pro Gln Pro
 565 570 575
 Ser Asp Glu Cys Thr Leu Leu Ser Asn Lys Tyr Leu Asp Gly Asn Ala

664674description (1)Sequence Listing

580

585

590

Asn Lys Ser Thr Ser Asp Gly Ser Pro Val Met Ala Val Met Pro Gly
 595 600 605

Thr Thr Asp Thr Ile Gln Val Leu Lys Gly Arg Met Asp Ser Glu Gln
 610 615 620

Ser Pro Ser Ile Gly Tyr Ser Ser Arg Thr Leu Gly Pro Asn Pro Gly
 625 630 635 640

Leu Ile Leu Gln Ala Leu Thr Leu Ser Asn Ala Ser Asp Gly Phe Asn
 645 650 655

Leu Glu Arg Leu Glu Met Leu Gly Asp Ser Phe Leu Lys His Ala Ile
 660 665 670

Thr Thr Tyr Leu Phe Cys Thr Tyr Pro Asp Ala His Glu Gly Arg Leu
 675 680 685

Ser Tyr Met Arg Ser Lys Lys Val Ser Asn Cys Asn Leu Tyr Arg Leu
 690 695 700

Gly Lys Lys Lys Gly Leu Pro Ser Arg Met Val Val Ser Ile Phe Asp
 705 710 715 720

Pro Pro Val Asn Trp Leu Pro Pro Gly Tyr Val Val Asn Gln Asp Lys
 725 730 735

Ser Asn Thr Asp Lys Trp Glu Lys Asp Glu Met Thr Lys Asp Cys Met
 740 745 750

Leu Ala Asn Gly Lys Leu Asp Glu Asp Tyr Glu Glu Glu Asp Glu Glu
 755 760 765

Glu Glu Ser Leu Met Trp Arg Ala Pro Lys Glu Glu Ala Asp Tyr Glu
 770 775 780

Asp Asp Phe Leu Glu Tyr Asp Gln Glu His Ile Arg Phe Ile Asp Asn
 785 790 795 800

Met Leu Met Gly Ser Gly Ala Phe Val Lys Lys Ile Ser Leu Ser Pro
 ページ(37)

664674description (1)Sequence Listing

805 Phe Ser Thr Thr Asp Ser Ala Tyr Glu Trp Lys Met Pro Lys Lys Ser
 820 825 830
 Ser Leu Gly Ser Met Pro Phe Ser Ser Asp Phe Glu Asp Phe Asp Tyr
 835 840 845
 Ser Ser Trp Asp Ala Met Cys Tyr Leu Asp Pro Ser Lys Ala Val Glu
 850 855 860
 Glu Asp Asp Phe Val Val Gly Phe Trp Asn Pro Ser Glu Glu Asn Cys
 865 870 875 880
 Gly Val Asp Thr Gly Lys Gln Ser Ile Ser Tyr Asp Leu His Thr Glu
 885 890 895
 Gln Cys Ile Ala Asp Lys Ser Ile Ala Asp Cys Val Glu Ala Leu Leu
 900 905 910
 Gly Cys Tyr Leu Thr Ser Cys Gly Glu Arg Ala Ala Gln Leu Phe Leu
 915 920 925
 Cys Ser Leu Gly Leu Lys Val Leu Pro Val Ile Lys Arg Thr Asp Arg
 930 935 940
 Glu Lys Ala Leu Cys Pro Thr Arg Glu Asn Phe Asn Ser Gln Gln Lys
 945 950 955 960
 Asn Leu Ser Val Ser Cys Ala Ala Ala Ser Val Ala Ser Ser Arg Ser
 965 970 975
 Ser Val Leu Lys Asp Ser Glu Tyr Gly Cys Leu Lys Ile Pro Pro Arg
 980 985 990
 Cys Met Phe Asp His Pro Asp Ala Asp Lys Thr Leu Asn His Leu Ile
 995 1000 1005
 Ser Gly Phe Glu Asn Phe Glu Lys Lys Ile Asn Tyr Arg Phe Lys
 1010 1015 1020
 Asn Lys Ala Tyr Leu Leu Gln Ala Phe Thr His Ala Ser Tyr His

664674description (1)Sequence Listing

1025		1030		1035	
Tyr Asn Thr Ile Thr Asp Cys Tyr Gln Arg Leu Glu Phe Leu Gly					
1040		1045		1050	
Asp Ala Ile Leu Asp Tyr Leu Ile Thr Lys His Leu Tyr Glu Asp					
1055		1060		1065	
Pro Arg Gln His Ser Pro Gly Val Leu Thr Asp Leu Arg Ser Ala					
1070		1075		1080	
Leu Val Asn Asn Thr Ile Phe Ala Ser Leu Ala Val Lys Tyr Asp					
1085		1090		1095	
Tyr His Lys Tyr Phe Lys Ala Val Ser Pro Glu Leu Phe His Val					
1100		1105		1110	
Ile Asp Asp Phe Val Gln Phe Gln Leu Glu Lys Asn Glu Met Gln					
1115		1120		1125	
Gly Met Asp Ser Glu Leu Arg Arg Ser Glu Glu Asp Glu Glu Lys					
1130		1135		1140	
Glu Glu Asp Ile Glu Val Pro Lys Ala Met Gly Asp Ile Phe Glu					
1145		1150		1155	
Ser Leu Ala Gly Ala Ile Tyr Met Asp Ser Gly Met Ser Leu Glu					
1160		1165		1170	
Thr Val Trp Gln Val Tyr Tyr Pro Met Met Arg Pro Leu Ile Glu					
1175		1180		1185	
Lys Phe Ser Ala Asn Val Pro Arg Ser Pro Val Arg Glu Leu Leu					
1190		1195		1200	
Glu Met Glu Pro Glu Thr Ala Lys Phe Ser Pro Ala Glu Arg Thr					
1205		1210		1215	
Tyr Asp Gly Lys Val Arg Val Thr Val Glu Val Val Gly Lys Gly					
1220		1225		1230	
Lys Phe Lys Gly Val Gly Arg Ser Tyr Arg Ile Ala Lys Ser Ala					

664674description (1)Sequence Listing

1235

1240

1245

Ala Ala Arg Arg Ala Leu Arg Ser Leu Lys Ala Asn Gln Pro Gln
 1250 1255 1260

Val Pro Asn Ser
 1265

<210> 19
 <211> 3804
 <212> DNA
 <213> Artificial

<220>
 <223> A gene encoding human dicer mutant

<400> 19
 atgaatcaca aagtgcacat tcatcatcat catatcgaag gtaggaattc gagctcggtta 60
 ccgcctcca ttgttgggcc accaatgagc tgtgtacgat tggctgaaag agttgtcgct 120
 ctcatattgct gtgagaaact gcacaaaatt ggcgaaactgg atgaccattt gatgccagtt 180
 gggaaagaga ctgttaaata tgaagaggag cttgatttgc atgatgaaga agagaccagt 240
 gttccaggaa gaccaggttc cacgaaacga aggcagtgc acccaaaagc aattccagag 300
 tgtttgaggg atagttatcc cagacctgat cagccctgtt acctgtatgt gataggaatg 360
 gttttaacta cacctttacc tgatgaactc aactttagaa ggcggaagct ctatcctcct 420
 gaagatacca caagatgctt tggaatactg acggccaaac ccataacctca gattccacac 480
 tttcctgtgt acacacgctc tggagagggt accatatcca ttgagttgaa gaagtctggt 540
 ttcatgttgt ctctacaaat gcttgagttg attacaagac ttcaccagta tatattctca 600
 catattcttc ggcttgaaaa acctgcacta gaatttaaac ctacagacgc tgattcagca 660
 tactgtgttc tacctcttaa tgttgttaat gactccagca ctttggatat tgactttaaa 720
 ttcatggaag atattgagaa gtctgaagct cgcataaggca ttcccagtac aaagtataca 780
 aaagaaacac cctttgtttt taaattagaa gattaccaag atgccgttat cattccaaga 840
 tatcgcaatt ttgatcagcc tcatcgattt tatgtagctg atgtgtacac tgatcttacc 900
 ccactcagta aatttccttc ccctgagtat gaaacttttg cagaatatta taaaacaaag 960
 tacaaccttg acctaaccac tctcaaccag ccactgctgg atgtggacca cacatcttca 1020
 agacttaatc ttttgacacc tcgacatttg aatcagaagg ggaaagcgct tcctttaago 1080

664674description (1)Sequence Listing

agtgctgaga agaggaaagc caaatgggaa agtctgcaga ataaacagat actggttcca	1140
gaactctgtg ctatacatcc aattccagca tcaactgtga gaaaagctgt ttgtctcccc	1200
agcatacttt atcgcccttca ctgccttttg actgcagagg agctaagagc ccagactgcc	1260
agcgatgctg gcgtgggagt cagatcactt cctgcggatt ttagataccc taacttagac	1320
ttcgggtgga aaaaatctat tgacagcaaa tctttcatct caatttctaa ctctcttca	1380
gotgaaaatg ataattactg taagcacagc acaattgtcc ctgaaaatgc tgcacatcaa	1440
gggtgctaata gaacctcctc tctagaaaat catgacaaaa tgtctgtgaa ctgcagaacg	1500
ttgtcagcg agtccctgg taagctccac gttgaagttt cagcagatct tacagcaatt	1560
aatggctctt cttacaatca aaatctcgcc aatggcagtt atgatttagc taacagagac	1620
ttttgccaag gaaatcagct aaattactac aagcaggaaa taccgctgca accaactacc	1680
tcatattcca ttcagaattt atacagttac gagaaccagc cccagcccag cgatgaatgt	1740
actctctga gtaataaata ccttgatgga aatgctaaca aatctacctc agatggaagt	1800
cctgtgatgg ccgtaatgcc tggtacgaca gacactattc aagtgtcaa gggcaggatg	1860
gattctgagc agagcccttc tattgggtac tcctcaagga ctcttgccc caatcctgga	1920
cttattcttc aggctttgac tctgtcaaac gctagtgatg gatttaacct ggagcggctt	1980
gaaatgcttg gcgactcctt tttaaagcat gccatcacca catatctatt ttgcacttac	2040
cctgatgcgc atgagggccg cctttcatat atgagaagca aaaaggctcag caactgtaat	2100
ctgtatcgcc ttggaaaaaa gaagggacta cccagccgca tgggtggtgtc aatatttgat	2160
ccccctgtga atttgcttcc tcctggttat gtagtaaato aagacaaaag caacacagat	2220
aaatgggaaa aagatgaaat gacaaaagac tgcatgctgg cgaatggcaa actggatgag	2280
gattacgagg aggaggatga ggaggaggag agcctgatgt ggagggtcc gaaggaagag	2340
gctgactatg aagatgattt cctggagtat gatcaggaac atatcagatt tatagataat	2400
atgttaatgg ggtcaggagc ttttgtaaag aaaatctctc tttctcctt ttcaaccact	2460
gattctgcat atgaatggaa aatgccc aaaatcctcct taggtagtat gccattttca	2520
tcagattttg aggattttga ctacagctct tgggatgcaa tgtgctatct ggatcctagc	2580
aaagctgttg aagaagatga ctttgtgtg gggttctgga atccatcaga agaaaactgt	2640
ggtgttgaca cgggaaagca gtccatttct tacgacttgc aactgagca gtgtattgct	2700
gacaaaagca tagcggactg tgtggaagcc ctgctgggct gctatttaac cagctgtggg	2760

664674description (1)Sequence Listing

gagagggctg ctcagctttt cctctgttca ctggggctga aggtgctccc ggtaattaaa	2820
aggactgata gggaaaaggc cctgtgccct actcgggaga atttcaacag ccaacaaaag	2880
aacctttcag tgagctgtgc tgctgcttct gtggccagtt cacgctcttc tgtattgaaa	2940
gactcggaat atggttgttt gaagattcca ccaagatgta tgtttgatca tccagatgca	3000
gataaaacac tgaatcacct tatatcgggg ttgaaaatt ttgaaaagaa aatcaactac	3060
agattcaaga ataaggctta ccttctccag gcttttacac atgcctccta ccactacaat	3120
actatcactg attgttacca gcgcttagaa ttccctgggag atgcgatttt ggactacctc	3180
ataaccaago acctttatga agaccgcggg cagcactccc cgggggtcct gacagacctg	3240
cggtctgccc tggtoaacaa caccatcttt gcatcgctgg ctgtaaagta cgactaccac	3300
aagtacttca aagctgtctc tcctgagctc ttccatgtca ttgatgactt tgtgcagttt	3360
cagcttgaga agaatgaaat gcaaggaatg gattctgagc ttaggagatc tgaggaggat	3420
gaagagaaaag aagaggatat tgaagttcca aaggccatgg gggatatttt tgagtcgctt	3480
gctgggtgcc tttacatgga tagtgggatg tccactggaga cagtctggca ggtgtactat	3540
cccatgatgc ggccactaat agaaaagttt tctgcaaag taccocgttc cctgtgoga	3600
gaattgcttg aaatggaacc agaaactgcc aaatttagcc cggctgagag aacttacgac	3660
gggaaggatc gagtactgt ggaagtagta ggaaagggga aatttaaagg tgttggtoga	3720
agttacagga ttgccaaatc tgcagcagca agaagagccc tccgaagcct caaagcta	3780
caacctcagg ttcccaatag ctaa	3804

<210> 20
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic primer rsGFP-F to amplify a gene encoding rsGFP

<400> 20
 gccacaacat tgaagatgga

20

<210> 21
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <223> Synthetic primer rsGFP-R to amplify a gene encoding rsGFP

664674description (1)Sequence Listing

<400> 21
 gaaagggcag attgtgtgga 20

 <210> 22
 <211> 20
 <212> DNA
 <213> Artificial

 <220>
 <223> Synthetic primer Neo-F to amplify a gene encoding Neo

 <400> 22
 atagcgttgg ctaccgtga 20

 <210> 23
 <211> 20
 <212> DNA
 <213> Artificial

 <220>
 <223> Synthetic primer Neo-R to amplify a gene encoding Neo

 <400> 23
 gaaggcgata gaaggcgatg 20

 <210> 24
 <211> 42
 <212> DNA
 <213> Artificial

 <220>
 <223> Synthetic primer dsl-1 to amplify a gene encoding luciferase

 <400> 24
 gggtaatagc actcactata gggagaatgg aagacgccaa aa 42

 <210> 25
 <211> 42
 <212> DNA
 <213> Artificial

 <220>
 <223> Synthetic primer dsl-2 to amplify a gene encoding luciferase

 <400> 25
 gggtaatagc actcactata gggagagaac gtgtacatcg ac 42

 <210> 26
 <211> 34
 <212> DNA

664674description (1)Sequence Listing

<213> Artificial

<220>

<223> Synthetic primer E to amplify a gene encoding CspB

<400> 26

gagcggataa catatgagag gaaaggtaa gtgg

34

<210> 27

<211> 37

<212> DNA

<213> Artificial

<220>

<223> Synthetic primer F to amplify a gene encoding CspB

<400> 27

gagcggataa ggatccttac tcaactactt tcacgtg

37